## SEQUENCE LISTING

<110> Gendaq Limited
<120> Screening System
<130> 674538-2003
<150> PCT/GB99/03730 <151> 1999-11-09
<150> GB9824544.2 <151> 1998-11-09
<160> 16
<170> PatentIn version 3.0
<210> 1 <211> 264 <212> DNA <213> Artificial Sequence
<220> <221> misc_structure <222> (1)(264) <223> sequence coding for a zinc finger protein
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cttacccgcc acacgaggac ccacacaggc gagaagcctt ttcagtgtcg aatctgcatg 120
cgtaacttca gcaggagcga taaccttacg agacacctaa ggacccacac aggcgagaag 180
ccttttcagt gtcgaatctg catgcgtaac ttcaggcaag ctgatcatct tcaagagcac 240
ctaaagaccc acacaggcga gaag 264
<210> 2 <211> 88 <212> PRT <213> Artificial Sequence
<220> <221> ZN_FING <222> (1)(88) <223> protein sequence encoding a zinc-finger domain
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Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser 1 5 10 15

Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His Leu Lys Thr His Thr Gly Glu Lys <210> 3 <211> 31 <212> PRT <213> Artificial Sequence <220> <221> VARIANT <222> (1)..(31) <223> 'X' can be any amino acid as described in the specification <400> 3 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa His Xaa Xaa Xaa Xaa Xaa Xaa His <210> 4 <211> 31 <212> PRT <213> Artificial Sequence <220> <221> VARIANT <222> (1)..(31) <223> 'X' can be any amino acid as described in the specification <400> 4 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Cys <210> 5 <211> 24 <212> PRT <213> Artificial Sequence

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<220>
<221> VARIANT
<222> (1)..(24)
<223> 'X' can be any amino acid as described in the specification
<400> 5
Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa
Leu Xaa Xaa His Xaa Xaa His
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Thr Gly Glu Lys
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Thr Gly Glu Lys Pro
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Leu Val Lys His Gln Arg Thr His Thr Gly
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Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
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<222> (1)..(6)
<223> leader peptide
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Met Ala Glu Glu Lys Pro
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<213> Artificial Sequence
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<222> (1)..(4)
<223> smallest unit of stalling polypeptide sequence
<400> 11
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Ala Ala Val Pro
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    Gly Gly Ser Ala Ala Val Pro
Ū
     <210> 13
J
     <211> 23
tū
     <212> DNA
m
     <213> Artificial Sequence
ļi
ſIJ
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     <221> promoter
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     <223> bacteriophage T7 RNA polymerase promoter sequence
Ü
I
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     taatacgact aactataggg aga
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      <213> Artificial Sequence
      <220>
      <221> PEPTIDE
      <222> (1)..(6)
      <223> ribosome stalling peptide sequence
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The first of the deep deep to the first
      Met Val Lys Thr Asp Lys
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The first first divite drive their street state
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18

<220>

## SEQUENCE LISTING

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<120> Screening System
<130> p3755
<140>
<141>
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<170> PatentIn Ver. 2.1
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Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
                                                          15
  1
                 . 5
                                                                    96
gat cgt agt agt ctt acc cgc cac acg agg acc cac aca ggc gag aag
Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
             20
                                  25
                                                      30
cct ttt cag tgt cga atc tgc atg cgt aac ttc agc agg agc gat aac
Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
                              40
         35
                                                                    192
ctt acg aga cac cta agg acc cac aca ggc gag aag cct ttt cag tgt
Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
     50
                          55
                                              60
cga atc tgc atg cgt aac ttc agg caa gct gat cat ctt caa gag cac
Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
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 65
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cta aag acc cac aca ggc gag aag Leu Lys Thr His Thr Gly Glu Lys 85

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<212> PRT

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 2

Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser

Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys 25 20

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn 40 35

Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys 60 55 50

Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His 80 75 70 65

Leu Lys Thr His Thr Gly Glu Lys 85